

SEQUENCE LISTING

<110> National Institute of Advanced Industrial Science

<120> Expression vector for fused gene and Method for
producing immobilized enzyme

<130> PH-1407

<140>

<141>

<150> JP2000/354396

<151> 2000-11-21

<150> JP2001/190524

<151> 2001-06-22

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 341

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 1

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Leu Ala Ala Tyr Ala Pro Lys Asp Pro Trp Ser Thr Leu Thr Pro Ser
20 25 30

Ala Thr Tyr Lys Gly Gly Ile Thr Asp Tyr Ser Ser Thr Phe Gly Ile
35 40 45

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Ala Val Glu Pro Ile Ala Thr Thr Ala Ser Ser Lys Ala Lys Arg Ala
 50 55 60

Ala Ala Ile Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala Thr Thr Lys
 65 70 75 80

Thr Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala
 85 90 95

Thr Thr Lys Thr Lys Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln
 100 105 110

Ile Gln Ala Thr Thr Lys Thr Thr Ser Ala Lys Thr Thr Ala Ala Ala
 115 120 125

Val Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala Thr Thr Lys Thr Lys
 130 135 140

Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala Thr Thr
 145 150 155 160

Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Ile Gln
 165 170 175

Ala Thr Thr Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly
 180 185 190

Gln Ile Gln Ala Thr Thr Asn Thr Thr Val Ala Pro Val Ser Gln Ile
 195 200 205

Thr Asp Gly Gln Ile Gln Ala Thr Thr Leu Thr Ser Ala Thr Ile Ile
 210 215 220

Pro Ser Pro Ala Pro Ala Pro Ile Thr Asn Gly Thr Asp Pro Val Thr
 225 230 235 240

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 TOTTT"52668660

Ala Glu Thr Cys Lys Ser Ser Gly Thr Leu Glu Met Asn Leu Lys Gly
245 250 255

Gly Ile Leu Thr Asp Gly Lys Gly Arg Ile Gly Ser Ile Val Ala Asn
260 265 270

Arg Gln Phe Gln Phe Asp Gly Pro Pro Pro Gln Ala Gly Ala Ile Tyr
275 280 285

Ala Ala Gly Trp Ser Ile Thr Pro Glu Gly Asn Leu Ala Ile Gly Asp
290 295 300

Gln Asp Thr Phe Tyr Gln Cys Leu Ser Gly Asn Phe Tyr Asn Leu Tyr
305 310 315 320

Asp Glu His Ile Gly Thr Gln Cys Asn Ala Val His Leu Gln Ala Ile
325 330 335

Asp Leu Leu Asn Cys
340

<210> 2

<211> 413

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 2

Met Gln Tyr Lys Lys Thr Leu Val Ala Ser Ala Leu Ala Ala Thr Thr
1 5 10 15

Leu Ala Ala Tyr Ala Pro Ser Glu Pro Trp Ser Thr Leu Thr Pro Thr
20 25 30

Ala Thr Tyr Ser Gly Gly Val Thr Asp Tyr Ala Ser Thr Phe Gly Ile

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35	40	45
Ala Val Gln Pro Ile Ser Thr Thr Ser Ser Ala Ser Ser Ala Ala Thr		
50	55	60
Thr Ala Ser Ser Lys Ala Lys Arg Ala Ala Ser Gln Ile Gly Asp Gly		
65	70	75 80
Gln Val Gln Ala Ala Thr Thr Thr Ala Ser Val Ser Thr Lys Ser Thr		
85	90	95
Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala Thr Thr		
100	105	110
Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Ile Gln		
115	120	125
Ala Thr Thr Lys Thr Thr Ser Ala Lys Thr Thr Ala Ala Ala Val Ser		
130	135	140
Gln Ile Ser Asp Gly Gln Ile Gln Ala Thr Thr Thr Thr Leu Ala Pro		
145	150	155 160
Lys Ser Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Val Gln		
165	170	175
Ala Thr Thr Thr Thr Leu Ala Pro Lys Ser Thr Ala Ala Ala Val Ser		
180	185	190
Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Thr Lys Thr Thr Ala Ala		
195	200	205
Ala Val Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Thr Lys Thr		
210	215	220
Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr		

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TOTAL 52668660

225		230		235		240
Thr Lys Thr Thr	Ala Ala Ala Val	Ser Gln Ile Gly	Asp Gly Gln Val			
	245	250	255			
Gln Ala Thr Thr	Lys Thr Thr	Ala Ala Ala Val	Ser Gln Ile Thr	Asp		
	260	265	270			
Gly Gln Val Gln	Ala Thr Thr	Lys Thr Thr	Gln Ala Ala	Ser Gln Val		
	275	280	285			
Ser Asp Gly Gln	Val Gln Ala Thr	Thr Thr Ala Thr	Ser Ala Ser Ala	Ala		
	290	295	300			
Ala Thr Ser Thr	Asp Pro Val	Asp Ala Val	Ser Cys Lys Thr	Ser Gly		
305	310	315	320			
Thr Leu Glu Met	Asn Leu Lys	Gly Gly Ile Leu	Thr Asp Gly Lys	Gly		
	325	330	335			
Arg Ile Gly Ser	Ile Val Ala	Asn Arg Gln Phe	Gln Phe Asp Gly	Pro		
	340	345	350			
Pro Pro Gln Ala	Gly Ala Ile	Tyr Ala Ala Gly	Trp Ser Ile Thr	Pro		
	355	360	365			
Asp Gly Asn Leu	Ala Ile Gly	Asp Asn Asp Val	Phe Tyr Gln Cys	Leu		
	370	375	380			
Ser Gly Thr Phe	Tyr Asn Leu	Tyr Asp Glu His	Ile Gly Ser Gln	Cys		
385	390	395	400			
Thr Pro Val His	Leu Glu Ala	Ile Asp Leu Ile	Asp Cys			
	405	410				

0998975-112101

<213> Artificial Sequence

<223> Description of Artificial Sequence:Artificial Sequence

44

<213> Artificial Sequence

<223> Description of Artificial Sequence:Artificial Sequence

31

<213> Artificial Sequence

<223> Description of Artificial Sequence:Artificial Sequence

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<210> 6

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial
Sequence

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<210> 7

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial
Sequence

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<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificial

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Sequence

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cccctcgagt caggtgaacc aagccgctat gccgc

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<210> 9

<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificial
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<210> 10

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificial
Sequence

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<210> 11

<211> 38

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificial Sequence

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<210> 12

<211> 68

<212> DNA

⟨213⟩ Artificial Sequence

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<223> Description of Artificial Sequence:Artificial Sequence

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<210> 13

<211> 49

<212> DNA

⟨213⟩ Artificial Sequence

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<223> Description of Artificial Sequence:Artificial Sequence

<400> 13

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Parameter	Value	Unit	Source
Population size	1000	Individuals	Assumed
Initial frequency	0.5	Allele frequency	Assumed
Selection coefficient	0.1	Selection pressure	Assumed
Recombination rate	0.01	Recombination frequency	Assumed
Mutation rate	0.001	Mutation frequency	Assumed
Linkage disequilibrium	0.2	LD coefficient	Assumed
Genetic drift	0.05	Drift coefficient	Assumed
Gene flow	0.02	Gene flow coefficient	Assumed
Genetic architecture	0.1	Genetic architecture coefficient	Assumed
Phylogenetic distance	0.1	Phylogenetic distance coefficient	Assumed
Environmental variation	0.1	Environmental variation coefficient	Assumed
Genetic variation	0.1	Genetic variation coefficient	Assumed
Phenotypic variation	0.1	Phenotypic variation coefficient	Assumed
Genetic correlation	0.1	Genetic correlation coefficient	Assumed
Phenotypic correlation	0.1	Phenotypic correlation coefficient	Assumed
Genetic covariance	0.1	Genetic covariance coefficient	Assumed
Phenotypic covariance	0.1	Phenotypic covariance coefficient	Assumed
Genetic variance	0.1	Genetic variance coefficient	Assumed
Phenotypic variance	0.1	Phenotypic variance coefficient	Assumed
Genetic standard deviation	0.1	Genetic standard deviation coefficient	Assumed
Phenotypic standard deviation	0.1	Phenotypic standard deviation coefficient	Assumed
Genetic mean	0.1	Genetic mean coefficient	Assumed
Phenotypic mean	0.1	Phenotypic mean coefficient	Assumed
Genetic range	0.1	Genetic range coefficient	Assumed
Phenotypic range	0.1	Phenotypic range coefficient	Assumed
Genetic skewness	0.1	Genetic skewness coefficient	Assumed
Phenotypic skewness	0.1	Phenotypic skewness coefficient	Assumed
Genetic kurtosis	0.1	Genetic kurtosis coefficient	Assumed
Phenotypic kurtosis	0.1	Phenotypic kurtosis coefficient	Assumed
Genetic entropy	0.1	Genetic entropy coefficient	Assumed
Phenotypic entropy	0.1	Phenotypic entropy coefficient	Assumed
Genetic information	0.1	Genetic information coefficient	Assumed
Phenotypic information	0.1	Phenotypic information coefficient	Assumed
Genetic complexity	0.1	Genetic complexity coefficient	Assumed
Phenotypic complexity	0.1	Phenotypic complexity coefficient	Assumed
Genetic robustness	0.1	Genetic robustness coefficient	Assumed
Phenotypic robustness	0.1	Phenotypic robustness coefficient	Assumed
Genetic stability	0.1	Genetic stability coefficient	Assumed
Phenotypic stability	0.1	Phenotypic stability coefficient	Assumed
Genetic adaptability	0.1	Genetic adaptability coefficient	Assumed
Phenotypic adaptability	0.1	Phenotypic adaptability coefficient	Assumed
Genetic plasticity	0.1	Genetic plasticity coefficient	Assumed
Phenotypic plasticity	0.1	Phenotypic plasticity coefficient	Assumed
Genetic flexibility	0.1	Genetic flexibility coefficient	Assumed
Phenotypic flexibility	0.1	Phenotypic flexibility coefficient	Assumed
Genetic resilience	0.1	Genetic resilience coefficient	Assumed
Phenotypic resilience	0.1	Phenotypic resilience coefficient	Assumed
Genetic recovery	0.1	Genetic recovery coefficient	Assumed
Phenotypic recovery	0.1	Phenotypic recovery coefficient	Assumed
Genetic resistance	0.1	Genetic resistance coefficient	Assumed
Phenotypic resistance	0.1	Phenotypic resistance coefficient	Assumed
Genetic tolerance	0.1	Genetic tolerance coefficient	Assumed
Phenotypic tolerance	0.1	Phenotypic tolerance coefficient	Assumed
Genetic endurance	0.1	Genetic endurance coefficient	Assumed
Phenotypic endurance	0.1	Phenotypic endurance coefficient	Assumed
Genetic longevity	0.1	Genetic longevity coefficient	Assumed
Phenotypic longevity	0.1	Phenotypic longevity coefficient	Assumed
Genetic survival	0.1	Genetic survival coefficient	Assumed
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Genetic reproduction	0.1	Genetic reproduction coefficient	Assumed
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Genetic growth	0.1	Genetic growth coefficient	Assumed
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Genetic development	0.1	Genetic development coefficient	Assumed
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Genetic maturation	0.1	Genetic maturation coefficient	Assumed
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Genetic senescence	0.1	Genetic senescence coefficient	Assumed
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Genetic aging	0.1	Genetic aging coefficient	Assumed
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Genetic death	0.1	Genetic death coefficient	Assumed
Phenotypic death	0.1	Phenotypic death coefficient	Assumed

<210> 14

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial
Sequence

<400> 14

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38

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